C E E a	Changed a file from non-ASCII to ASCII Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The humbar inputted by the applicant was the prior application data; or other	
E a	Edited a format error in the Current Application Data section, specifically:	
E a		
	Edited the Current Application Data section with the actual surrent sumbale Alice	
	applicant was the prior application data; or other	
Α	Added the mandatory heading and subheadings for "Current Application Data".	
E	Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.	
	Changed the spelling of a mandatory field (the headings or subheadings), specifically:	
С	Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:	
	nserted or corrected a nucleic number at the end of a nucleic line. SEQUENO's edited:	
	corrected subheading placement. All responses must be on the same line as each subheading. If the pplicant placed a response below the subheading, this was moved to its appropriate place.	
lr	nserted colons after headings/subheadings. Headings edited included:	
D	Deleted extra, invalid, headings used by an applicant, specifically:	
	Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file page numbers throughout text; ☐ other invalid text, such as	
ĺ	Inserted mandatory headings, specifically:	
C	Corrected an obvious error in the response, specifically:	
 E	Edited identifiers where upper case is used but lower case is required, or vice versa.	
C	Corrected an error in the Number of Sequences field, specifically:	
	A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.	
	eleted <i>ending</i> stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error use to a PatentIn bug). Sequences corrected:	
C	Other:	

^{*}Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PAGÉ: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/902,516

DATE: 11/23/98 TIME: 12:08:42

INPUT SET: S29984.raw

J. Spector

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

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Does Not Comply
                                                                Corrected Diskette Needed
 1
                                       SEQUENCE LISTING
 2
 3
    (1)
            General Information:
 5
          (i) APPLICANT: Soo Hoo, William
 6
 7
         (ii) TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
 8
          COMPRISING GM-CSF ANDMETHODS OF MODULATING AN IMMUNE
 9
         RESPONSE USING SAME
10
11
        (iii) NUMBER OF SEQUENCES: 50
12
13
         (iv) CORRESPONDENCE ADDRESS:
14
               (A) ADDRESSEE: CAMPBELL & FLORES, LLP
15
               (B) STREET: 4370 La Jolla Village Drive, Suite 700
16
               (C) CITY: San Diego
17
               (D) STATE: California
18
               (E) COUNTRY: United States
19
               (F) ZIP: 92121
20
21
          (v) COMPUTER READABLE FORM:
22
               (A) MEDIUM TYPE: Floppy disk
               (B) COMPUTER: IBM PC compatible
23
24
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27
         (vi) CURRENT APPLICATION DATA:
               (A) APPLICATION NUMBER: US 08/902,516
28
               (B) FILING DATE: 29-JUL-1997
29
30
               (C) CLASSIFICATION:
31
32
       (viii) ATTORNEY/AGENT INFORMATION:
33
               (A) NAME: Campbell, Cathryn A.
34
               (B) REGISTRATION NUMBER: 31,815
35
               (C) REFERENCE/DOCKET NUMBER: P-IM 2442
36
37
         (ix) TELECOMMUNICATION INFORMATION:
               (A) TELEPHONE: (619)535-9001
39
               (B) TELEFAX: (619)535-8949
40
```

ERRORED SEQUENCES FOLLOW:

41

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/08/902,516

DATE: 11/23/98 TIME: 12:08:43

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(2) INFORMATION FOR SEQ ID NO:1:
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43
44
          (i) SEQUENCE CHARACTERISTICS:
45
               (A) LENGTH: 660 base pairs
               (B) TYPE: nucleic acid
46
47
               (C) STRANDEDNESS: both
               (D) TOPOLOGY: linear
48
49
50
         (ix) FEATURE:
51
52
               (A) NAME/KEY: CDS
                                                                       fornet eva
53
               (B) LOCATION: 1..660
54
55
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57
58
    ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA
59
60
    Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Trp Val Pro
61
62
    GGT TCC ACT GGG GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC
63
64
65
    Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
66
                  20
                                      25
                                                           30
67
68
    CAA GCA CCC ACC CGC TCA CCC ATC ACT GTC ACC CGG CCT TGG AAG CAT
69
70
    Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His
71
72
73
    GTA GAG GCC ATC AAA GAA GCC CTG AAC CTC CTG GAT GAC ATG CCT GTC
74
    192
75
    Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val
76
77
78
    ACG TTG AAT GAA GAG GTA GAA GTC GTC TCT AAC GAG TTC TCC TTC AAG
79
80
    Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys
81
                          70
                                               75
                                                                   80
82
83
    AAG CTA ACA TGT GTG CAG ACC CGC CTG AAG ATA TTC GAG CAG GGT CTA
84
    Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu
85
86
87
88
    CGG GGC AAT TTC ACC AAA CTC AAG GGC GCC TTG AAC ATG ACA GCC AGC
89
90
    Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser
91
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                                     105
92
93
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94
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PAGE: 3

RAW SEQUENCE LISTING PATENT APPLICATION US/08/902,516

DATE: 11/23/98 TIME: 12:08:45

95 Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp 96	ACC TTT CTG Thr Phe Leu	
97 98 CAA GTT ACC ACC TAT GCG GAT TTC ATA GAC AGC CTT AAA 99 432 100 Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys 101 130 135 140 102 103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170	ACC TTT CTG Thr Phe Leu	
98 CAA GTT ACC ACC TAT GCG GAT TTC ATA GAC AGC CTT AAA 99 432 100 Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys 101 130 135 140 102 103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170	Thr Phe Leu	
99 432 100 Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys 101 130 135 140 102 103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170	Thr Phe Leu	
100 Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys 101 130 135 140 102 103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170		
101 130 135 140 102 103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170		
102 103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170	GTC GAC GAA	
103 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA 104 480 105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170	ርጥሮ ርልሮ ርልል	
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105 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys 106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170 112	OIC ONC ONN	
106 145 150 155 107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170 112		
107 108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170 112	Val Asp Glu	
108 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC 109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170 112	160	
109 528 110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170 112		
110 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly 111 165 170 112	CAG GAC ACG	
111 165 170 112		
112	-	
	175	
113 - ሮእር ርእር ርጥሮ እጥሮ ርጥር ርጥር ሮሊን ሮእር ጥሮር ጥጥር ሮሮር ጥጥጥ አእር		
	GTG GTG GTG	
114 576		
115 Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys		
116 180 185	190	
117		
118 ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC ATC ATC	TCC CTT ATC	
119 624		
120 Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile		
121 195 200 205		
122		
> 123 ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT TAG	660	
124 Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg		
125 210 215 220		
126		
127		

PAGE: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION *US/08/902,516*

DATE: 11/23/98 TIME: 12:08:46

INPUT SET: S29984.raw

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45 123	Entered (660) and Calc. Seq. Length (36) differ # of Sequences for line conflicts w/ running total	(A) LENGTH: 660 base pairs ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CG